

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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			20					25					30		
Arg	Ser	Leu	Pro	Glu	Asn	Ile	Gln	Phe	Asp	Val	Tyr	Tyr	Lys	Leu	Tyr
		35					40					45			
Gln	Gln	Gly	Arg	Leu	Cys	Gln	Leu	Gly	Ser	Glu	Phe	Cys	Glu	Leu	Glu
	50				55					60					
Val	Phe	Ala	Lys	Val	Leu	Arg	Ala	Leu	Asp	Lys	Arg	His	Leu	Leu	His
65				70					75					80	
His	Cys	Phe	Gln	Ala	Leu	Met	Asp	His	Gly	Val	Lys	Val	Ala	Ser	Val
			85						90					95	
Leu	Ala	Tyr	Ser	Phe	Ser	Arg	Arg	Cys	Ser	Tyr	Ile	Ala	Glu	Ser	Asp
			100					105					110		
Ala	Ala	Val	Lys	Glu	Lys	Ala	Ile	Gln	Val	Gly	Phe	Val	Leu	Gly	Gly
		115					120					125			
Phe	Leu	Ser	Asp	Ala	Gly	Trp	Tyr	Ser	Asp	Ala	Glu	Lys	Val	Phe	Leu
	130				135					140					
Ser	Cys	Leu	Gln	Leu	Cys	Thr	Leu	His	Asp	Glu	Met	Leu	His	Trp	Phe
145				150					155					160	
Arg	Ala	Val	Glu	Cys	Cys	Val	Arg	Leu	Leu	His	Val	Arg	Asn	Gly	Asn
			165					170					175		
Cys	Lys	Tyr	His	Leu	Gly	Glu	Glu	Thr	Phe	Lys	Leu	Ala	Gln	Thr	Tyr
		180				185						190			
Met	Asp	Lys	Leu	Ser	Lys	His	Gly	Gln	Gln	Ala	Asn	Lys	Ala	Ala	Leu
	195					200						205			
Tyr	Gly	Glu	Leu	Cys	Ala	Leu	Leu	Phe	Ala	Lys	Ser	His	Tyr	Asp	Glu
	210				215						220				

Ala Tyr Lys Trp Cys Ile Glu Ala Met Lys Glu Ile Thr Ala Gly Leu
 225 230 235 240
 Pro Val Lys Val Val Val Asp Val Leu Arg Gln Ala Ser Lys Ala Cys
 245 250 255
 Val Val Lys Arg Glu Phe Lys Lys Ala Glu Gln Leu Ile Lys His Ala
 260 265 270
 Val Tyr Leu Ala Arg Asp His Phe Gly Ser Lys His Pro Lys Tyr Ser
 275 280 285
 Asp Thr Leu Leu Asp Tyr Gly Phe Tyr Leu Leu Asn Val Asp Asn Ile
 290 295 300
 Cys Gln Ser Val Ala Ile Tyr Gln Ala Ala Leu Asp Ile Arg Gln Ser
 305 310 315 320
 Val Phe Gly Gly Lys Asn Ile His Val Ala Thr Ala His Glu Asp Leu
 325 330 335
 Ala Tyr Ser Ser Tyr Val His Gln Tyr Ser Ser Gly Lys Phe Asp Asn
 340 345 350
 Ala Leu Phe His Ala Glu Arg Ala Ile Gly Ile Ile Thr His Ile Leu
 355 360 365
 Pro Glu Asp His Leu Leu Leu Ala Ser Ser Lys Arg Val Lys Ala Leu
 370 375 380
 Ile Leu Glu Glu Ile Ala Ile Asp Cys His Asn Lys Glu Thr Glu Gln
 385 390 395 400
 Arg Leu Leu Gln Glu Ala His Asp Leu His Leu Ser Ser Leu Gln Leu
 405 410 415
 Ala Lys Lys Ala Phe Gly Glu Phe Asn Val Gln Thr Ala Lys His Tyr
 420 425 430
 Gly Asn Leu Gly Arg Leu Tyr Gln Ser Met Arg Lys Phe Lys Glu Ala
 435 440 445
 Glu Glu Met His Ile Lys Ala Ile Gln Ile Lys Glu Gln Leu Leu Gly
 450 455 460
 Gln Glu Asp Tyr Glu Val Ala Leu Ser Val Gly His Leu Ala Ser Leu
 465 470 475 480
 Tyr Asn Tyr Asp Met Asn Gln Tyr Glu Asn Ala Glu Lys Leu Tyr Leu
 485 490 495
 Arg Ser Ile Ala Ile Gly Lys Lys Leu Phe Gly Glu Gly Tyr Ser Gly
 500 505 510
 Leu Glu Tyr Asp Tyr Arg Gly Leu Ile Lys Leu Tyr Asn Ser Ile Gly
 515 520 525
 Asn Tyr Glu Lys Val Phe Glu Tyr His Asn Val Leu Ser Asn Trp Asn
 530 535 540
 Arg Leu Arg Asp Arg Gln Tyr Ser Val Thr Asp Ala Leu Glu Asp Val
 545 550 555 560
 Ser Thr Ser Pro Gln Ser Thr Glu Glu Val Val Gln Ser Phe Leu Ile
 565 570 575
 Ser Gln Asn Val Glu Gly Pro Ser Cys
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<210> 2

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 2

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tttgatgttt actacaagct ttaccaacag ggacgcttat gtcaactggg cagtgaattt      180
tgtgaattgg aagtttttgc taaagtactg agagctttgg ataaaagaca tttgcttcat      240

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caggttggct ttgttttagg tggctttctt tcagatgcag gctggtacag tgatgctgag 420
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ttgggtgaag aaacatttaa attagctcag acatatatgg ataaactatc aaaacatggc 600
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ccagtgaag ttgtggtgga tgtcttaaga caagcttcta aggcttgtgt agtaaaacgt 780
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tctaactgga accggttgcg agatcggcaa tattcagtga cagatgctct tgaagatgtc 1680
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gagggaccga gctgctga 1758

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<210> 3

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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 20          25          30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35          40          45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
 50          55          60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
 65          70          75          80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
 85          90          95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
100          105          110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
115          120          125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
130          135          140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145          150          155          160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
165          170          175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
180          185          190

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Gln	Gln	Gln	Gln	Gln	Glu	Ala	Val	Ser	Glu	Gly	Ser	Ser	Ser	Gly	Arg
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Ala	Arg	Glu	Ala	Ser	Gly	Ala	Pro	Thr	Ser	Ser	Lys	Asp	Asn	Tyr	Leu
	210					215					220				
Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala	Lys	Glu	Leu	Cys	Lys	Ala
225					230					235					240
Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser
				245					250					255	
Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu	Leu	Gly
			260				265						270		
Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala	Glu	Cys
		275					280					285			
Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu	Asp	Thr
	290					295					300				
Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly
305					310				315						320
Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr
				325					330					335	
Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp
			340					345					350		
Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala
		355					360					365			
Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	Ala	Arg
	370					375					380				
Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala
385				390					395						400
Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly
				405					410					415	
Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser
			420					425					430		
Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys
		435					440					445			
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	450					455					460				
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr
465					470				475						480
Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe
				485					490					495	
Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro
			500					505					510		
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp
		515					520					525			
Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp
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His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu
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Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys
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Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys
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Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg
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Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met
	610					615					620				
Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln
625					630				635						640
Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr
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Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile
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Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
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 Pro Ile Tyr Phe His Thr Gln
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<210> 4

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 4

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 cggcggcttc gaagccgccg cccggagctg ccctttcctc ttcggtgaag tttttaaaag 240
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<210> 5

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

Met	Ser	Gly	Arg	Pro	Arg	Thr	Thr	Ser	Phe	Ala	Glu	Ser	Cys	Lys	Pro
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Val	Gln	Gln	Pro	Ser	Ala	Phe	Gly	Ser	Met	Lys	Val	Ser	Arg	Asp	Lys
			20					25					30		
Asp	Gly	Ser	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Pro	Gly	Gln	Gly	Pro
		35					40					45			
Asp	Arg	Pro	Gln	Glu	Val	Ser	Tyr	Thr	Asp	Thr	Lys	Val	Ile	Gly	Asn
	50					55					60				
Gly	Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Lys	Leu	Cys	Asp	Ser	Gly	Glu
65				70				75							80
Leu	Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg
			85					90						95	
Glu	Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu
			100					105					110		
Arg	Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Val	Tyr	Leu
		115					120					125			
Asn	Leu	Val	Leu	Asp	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg
	130					135						140			
His	Tyr	Ser	Arg	Ala	Lys	Gln	Thr	Leu	Pro	Val	Ile	Tyr	Val	Lys	Leu
145				150						155					160
Tyr	Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Phe	Gly
			165					170						175	
Ile	Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Leu	Asp	Pro	Asp
			180					185					190		
Thr	Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val
		195					200					205			
Arg	Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala
	210					215					220				
Pro	Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val
225				230				235							240
Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile
			245					250						255	
Phe	Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val
		260						265					270		
Leu	Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr
		275				280						285			
Thr	Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Asp
	290					295					300				
Ser	Ser	Gly	Thr	Gly	His	Phe	Thr	Ser	Gly	Val	Arg	Val	Phe	Arg	Pro
305				310						315					320
Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Arg	Leu	Leu	Glu	Tyr
			325					330						335	
Thr	Pro	Thr	Ala	Arg	Leu	Thr	Pro	Leu	Glu	Ala	Cys	Ala	His	Ser	Phe
			340					345					350		
Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Val	Lys	Leu	Pro	Asn	Gly	Arg	Asp
	355					360						365			
Thr	Pro	Ala	Leu	Phe	Asn	Phe	Thr	Thr	Gln	Glu	Leu	Ser	Ser	Asn	Pro
	370					375					380				
Pro	Leu	Ala	Thr	Ile	Leu	Ile	Pro	Pro	His	Ala	Arg	Ile	Gln	Ala	Ala
385				390						395					400
Ala	Ser	Thr	Pro	Thr	Asn	Ala	Thr	Ala	Ala	Ser	Asp	Ala	Asn	Thr	Gly
			405					410						415	
Asp	Arg	Gly	Gln	Thr	Asn	Asn	Ala	Ala	Ser	Ala	Ser	Ala	Ser	Asn	Ser
			420					425						430	
Thr															

<210> 6
 <211> 1639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 6
 atcatctata tgttaaatat ccgtgccgat ctgtcttgaa ggagaaatat atcgcttggt 60
 ttgtttttta tagtatacaa aaggagtga aagccaagag gacgaagtct ttttcttttt 120
 cttctgtggg agaacttaat gctgcattta tcgttaacct aacaccccaa cataaagaca 180
 aaaggaagaa aaggaggaag gaaggaaaag gtgattcgcg aagagagtga tcatgtcagg 240
 gcggcccaga accacctcct ttgcggagag ctgcaagccg gtgcagcagc cttcagcttt 300
 tggcagcatg aaagttagca gagacaagga cggcagcaag gtgacaacag tgggtggcaac 360
 tcctgggagc ggtccagaca ggccacaaga agtcagctat acagacacta aagtgattgg 420
 aaatggatca tttggtgtgg tatatcaagc caaactttgt gattcaggag aactggtcgc 480
 catcaagaaa gtattgcagg acaagagatt taagaatcga gagctccaga tcatgagaaa 540
 gctagatcac tgtaacatag tccgattgag ttatttcttc tactccagtg gtgagaagaa 600
 agatgaggtc tatcttaatc tgggtgctgga ctatgttccg gaaacagtat acagagttgc 660
 cagacactat agtcgagcca aacagacgct ccctgtgatt tatgtcaagt tgtatatgta 720
 tcagctgttc cgaagttag cctatatcca ttcctttgga atctgccatc gggatattaa 780
 accgcagaac ctcttggttg atcctgatac tgctgtatta aaactctgtg actttggaag 840
 tgcaaagcag ctgggccgag gagaacccaa tgtttcgtat atctgttctc ggtactatag 900
 ggcaccagag ttgatctttg gagccactga ttatacctct agtatagatg tatggtctgc 960
 tggctgtgtg ttggctgagc tgttactagg acaaccaata tttccagggg atagtgggtg 1020
 ggatcagttg gtagaaataa tcaaggtcct gggaactcca acaagggagc aaatcagaga 1080
 aatgaacca aactacacag aatttaaatt ccctcaaatt aaggcacatc cttggactaa 1140
 ggattcgtca ggaacaggac atttcacctc aggagtgcgg gtcttccgac cccgaactcc 1200
 accggaggca attgcactgt gtagccgtct gctggagtat acaccaactg cccgactaac 1260
 accactggaa gcttgtgcac attcatTTTT tgatgaatta cgggacccaa atgtcaaact 1320
 accaaatggg cgagacacac ctgcactctt caacttcacc actcaagaac tgtcaagtaa 1380
 tccacctctg gctaccatcc ttattcctcc tcatgctcgg attcaagcag ctgcttcaac 1440
 cccacaaaat gccacagcag cgtcagatgc taatactgga gaccgtggac agaccaataa 1500
 tgctgcttct gcatcagctt ccaactccac ctgaacagtc ccgagcagcc agctgcacag 1560
 gaaaaaccac cagttacttg agtgtcactc agcaacactg gtcacgtttg gaaagaatat 1620
 taaaaaaaaa aaaaaaaaaa 1639

<210> 7
 <211> 391
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 7
 Met Lys Cys Leu Val Thr Gly Gly Asn Val Lys Val Leu Gly Lys Ala
 1 5 10 15
 Val His Ser Leu Ser Arg Ile Gly Asp Glu Leu Tyr Leu Glu Pro Leu
 20 25 30
 Glu Asp Gly Leu Ser Leu Arg Thr Val Asn Ser Ser Arg Ser Ala Tyr
 35 40 45
 Ala Cys Phe Leu Phe Ala Pro Leu Phe Phe Gln Gln Tyr Gln Ala Ala
 50 55 60
 Thr Pro Gly Gln Asp Leu Leu Arg Cys Lys Ile Leu Met Lys Ser Phe
 65 70 75 80

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
 85 90 95
 Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
 100 105 110
 His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
 115 120 125
 Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
 130 135 140
 Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
 145 150 155 160
 Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Arg Val
 165 170 175
 Ile Leu Arg Ser Tyr His Glu Glu Glu Ala Asp Ser Thr Ala Lys Ala
 180 185 190
 Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
 195 200 205
 Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
 210 215 220
 Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
 225 230 235 240
 Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
 245 250 255
 Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
 260 265 270
 Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
 275 280 285
 Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
 290 295 300
 Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
 305 310 315 320
 Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
 325 330 335
 Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
 340 345 350
 Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
 355 360 365
 Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
 370 375 380
 Glu Asp Ser Glu Gly Glu Gly
 385 390

<210> 8

<211> 2102

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8

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gcgcgggaag ggaccccgga cccggaggct gcggagagct gggcagtgtt ggccgctggc      60
ggagcgctgg ggcagcatga agtgccctgg caggggcggc aacgtgaagg tgctcggcaa      120
ggccgtccac tcctgtccc gcacgcggga cgagctctac ctggaaccct tggaggacgg      180
gctctccctc cggacggtga actcctcccg ctctgcctat gcttgctttc tctttgcccc      240
gctcttcttc cagcaatacc aggcagccac ccctggtcag gacctgctgc gctgtaagat      300
cctgatgaag tctttcctgt ctgtcttccg ctactggcg atgctggaga agacggtgga      360
aaaatgctgc atctccctga atggccggag cagccgcctg gtggtccagc tgcattgcaa      420
gttcgggggtg cggaagactc acaacctgtc cttccaggac tgtgagtccc tgcaggccgt      480
cttcgaccca gcctcgtgcc cccacatgct ccgcgccccca gcacgggttc tgggggaggc      540
tggttctgccc ttctctcctg cactggctga agtgacgctg ggcattggcc gtggccgcag      600

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ggtcacccctg cgcagctacc acgaggagga ggcagacagc actgccaaag ccatgggtgac 660
tgagatgtgc cttggagagg aggatttcca gcagctgcag gccaggaag ggggtggccat 720
cactttctgc ctcaaggaat tccggggggt cctgagcttt gcagagtcag caaacttgaa 780
tcttagcatt catthttgatg ctccaggcag gcccgccatc ttcaccatca aggactcttt 840
gctggacggc cactttgtct tggccacact ctcagacacc gactcgcact cccaggacct 900
gggctcccca gagcgtcacc agccagtgcc tcagctccag gctcacagca caccaccacc 960
ggacgacttt gccaatgacg acattgactc ttacatgac gccatggaaa ccactatagg 1020
caatgagggc tcgcgggtgc tgccctccat ttccctttca cctggccccc agccccccaa 1080
gagccccggg cccactccg aggaggaaga tgaggctgag ccagtacag tgcctgggac 1140
tccccaccc aagaagttcc gctcactgtt cttcggctcc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagtgag ggtgaaggct gaaccaagaa 1260
cctgaagcct gtaccagag gccttggaact agacgaagcc ccagccagtg gcagaactgg 1320
gtctctcagc cctggggatc agaaagggtg gcttgctgga gctgagctgt ttcactgcct 1380
ctcgcaggcc ccagctggct gtcactgtaa agctgtccca cagcggctcg gcctgggccc 1440
ttatctccc acaaccccca gccaatcagg actttccaga cttggccctg aactactgac 1500
gttctacct cttatttctc attgagcctc aggctatact ccagctggcc aaggctggaa 1560
acctgtctcc ctcaggctca ccttcctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gcttctctgc caatcatgac ctgttccttc ctgaagtcct gggcatgcat 1680
ctgggacccc cgtggagctg acaagttttc cttgctttcc tgatactctt tggcgctgac 1740
ttggaattct aagagccttg gacccgagtg tgtggctagg gttgccctgg ctggggcccg 1800
gtgccgagac tccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttatcc aagagaccag atgggttgcc 1920
ccaggatccg gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg caggtgcagg 2040
caggaagcag ccctggggga ctggacgctg ctattgattc attaaaaaaa gaaaagaaaa 2100
at 2102

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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

gggcccctgg atggatagct ac

22

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

gtagctatcc atccaggggc c

21

<210> 11

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

gggcccctgg atggatagct acctcgaggt agctatccat ccagggggcc

49

<210> 12

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

tttttggggcc cctggatgga tagctacctc gaggtagcta tccatccagg ggcc

54

<210> 13

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

Met	Ala	Thr	Ile	Glu	Glu	Ile	Ala	His	Gln	Ile	Ile	Glu	Gln	Gln	Met
1				5					10					15	
Gly	Glu	Ile	Val	Thr	Glu	Gln	Gln	Thr	Gly	Gln	Lys	Ile	Gln	Ile	Val
			20					25					30		
Thr	Ala	Leu	Asp	His	Asn	Thr	Gln	Gly	Lys	Gln	Phe	Ile	Leu	Thr	Asn
		35					40					45			
His	Asp	Gly	Ser	Thr	Pro	Ser	Lys	Val	Ile	Leu	Ala	Arg	Gln	Asp	Ser
	50					55					60				
Thr	Pro	Gly	Lys	Val	Phe	Leu	Thr	Thr	Pro	Asp	Ala	Ala	Gly	Val	Asn
65					70					75					80
Gln	Leu	Phe	Phe	Thr	Pro	Asp	Leu	Ser	Ala	Gln	His	Leu	Gln	Leu	
			85					90					95		
Leu	Thr	Asp	Asn	Ser	Pro	Asp	Gln	Gly	Pro	Asn	Lys	Val	Phe	Asp	Leu
			100					105					110		
Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Arg	His	Tyr	Gly	Ala	Val
		115					120					125			
Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Ser	Ile	Arg	Lys	Asn
	130					135					140				
Leu	Val	Tyr	Ser	Cys	Arg	Gly	Ser	Lys	Asp	Cys	Ile	Ile	Asn	Lys	His
145					150					155					160
His	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu	Gln	Arg	Cys	Ile	Ala	Phe
			165					170					175		
Gly	Met	Lys	Gln	Asp	Ser	Val	Gln	Cys	Glu	Arg	Lys	Pro	Ile	Glu	Val
			180					185					190		
Ser	Arg	Glu	Lys	Ser	Ser	Asn	Cys	Ala	Ala	Ser	Thr	Glu	Lys	Ile	Tyr
	195						200					205			
Ile	Arg	Lys	Asp	Leu	Arg	Ser	Pro	Leu	Thr	Ala	Thr	Pro	Thr	Phe	Val
	210					215					220				
Thr	Asp	Ser	Glu	Ser	Thr	Arg	Ser	Thr	Gly	Leu	Leu	Asp	Ser	Gly	Met
225					230					235					240
Phe	Met	Asn	Ile	His	Pro	Ser	Gly	Val	Lys	Thr	Glu	Ser	Ala	Val	Leu
			245						250					255	
Met	Thr	Ser	Asp	Lys	Ala	Glu	Ser	Cys	Gln	Gly	Asp	Leu	Ser	Thr	Leu
			260					265					270		
Ala	Asn	Val	Val	Thr	Ser	Leu	Ala	Asn	Leu	Gly	Lys	Thr	Lys	Asp	Leu
		275					280						285		

```

Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
 290                               295                               300
Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
305                               310                               315                               320
Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
                               325                               330                               335
Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
                               340                               345                               350
Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
                               355                               360                               365
Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
                               370                               375                               380
Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
385                               390                               395                               400
Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
                               405                               410                               415
Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
                               420                               425                               430
Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
                               435                               440                               445
Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
                               450                               455                               460
Asp Ala Lys Val Ile Ala Ala Leu Ile His Phe Thr Arg Arg Ala Ile
465                               470                               475                               480
Thr Asp Leu

```

<210> 14

<211> 596

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

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Met Thr Ser Pro Ser Pro Arg Ile Gln Ile Ile Ser Thr Asp Ser Ala
 1                               5                               10                               15
Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
                               20                               25                               30
Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
                               35                               40                               45
Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
                               50                               55                               60
Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
65                               70                               75                               80
Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
                               85                               90                               95
Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
                               100                               105                               110
Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
                               115                               120                               125
Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
                               130                               135                               140
Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
145                               150                               155                               160
Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
                               165                               170                               175
Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
                               180                               185                               190

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Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
   195                               200               205
Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
   210                               215               220
Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
  225                               230               235               240
Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
   245                               250               255
Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
   260                               265               270
Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
   275                               280               285
Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
   290                               295               300
Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
  305                               310               315               320
Asn Thr Thr Asp Ser Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
   325                               330               335
Thr Ser Gly Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
   340                               345               350
Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
   355                               360               365
Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
   370                               375               380
Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
  385                               390               395               400
Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
   405                               410               415
Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
   420                               425               430
Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
   435                               440               445
Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
   450                               455               460
Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
  465                               470               475               480
Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
   485                               490               495
Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
   500                               505               510
Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
   515                               520               525
Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
   530                               535               540
Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
  545                               550               555               560
Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
   565                               570               575
Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
   580                               585               590
Gly Ala Ser Leu
   595

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<210> 15

<211> 2029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

gaattcgggc	ccgtcggctt	tcttcaaccc	tctcttcccg	gagcgcccc	aatccacgag	60
tggcagccgc	gggactgtcg	cgtcggcgcc	cgacgcggag	tcagcagggg	cgaaaagcgg	120
tagatcatgg	caaccataga	agaaattgca	catcaaatta	ttgaacaaca	gatgggagag	180
attgttacag	agcagcaaac	tgggcagaaa	atccagattg	tgacagcact	tgatcataat	240
acccaaggca	agcagttcat	tctgacaaat	cacgacggct	ctactccaag	caaagtcatt	300
ctggccaggc	aagattccac	tccgggaaaa	gttttcctta	caactccaga	tgcagcaggt	360
gtcaaccagt	tattttttac	cactcctgat	ctgtctgcac	aacacctgca	gctcctaaca	420
gataattctc	cagaccaagg	accaaataag	gtttttgatc	tttgcgtagt	atgtggagac	480
aaagcatcag	gacgtcatta	tggagcagta	acttgtgaag	gctgcaaagg	atTTTTTaaa	540
agaagcatcc	gaaaaaatTT	agtataattca	tgtcgaggat	caaaggattg	tattattaat	600
aagcaccacc	gaaaccgctg	tcaatactgc	aggttacaga	gatgtattgc	gttttggaatg	660
aagcaagact	ctgtccaatg	tgaagaaaa	cccatggaag	tatcacgaga	aaaatcttcc	720
aactgtgccg	cttcaacaga	aaaaatctat	atccgaaagg	accttcgtag	cccatctaact	780
gcaactccaa	cttttgtaac	agatagtga	agtacaagg	caacaggact	gttagattca	840
ggaatgttca	tgaatattca	tccatctgga	gtaaaaactg	agtcagctgt	gctgatgaca	900
tcagataaagg	ctgaatcatg	tcaggagagat	ttaagtacat	tggccaatgt	ggttacatca	960
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actaatggat	gggtttttaa	catgtccctc	tacaataaat	taaaatcttt	caatgtttga	1980
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<210> 16

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

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<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

cgctgtaaga tcctgatgaa gtc

23

<210> 18

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

tgctctctcc tcgtggtag

19

<210> 19

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19
 tgccttcctt ggatgtggta g

21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
 cgtctgccct atcaactttc g

21

<210> 21
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 20 25 30
 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220

Tyr	Leu	Gly	Gly	Thr	Ser	Thr	Ile	Ser	Asp	Asn	Ala	Lys	Glu	Leu	Cys
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Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His
				245					250					255	
Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu
			260					265					270		
Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala
		275					280					285			
Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu
290					295						300				
Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu
305					310					315					320
Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser
				325				330						335	
Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala
		340						345					350		
Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro
	355						360					365			
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	370					375						380			
Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala
385					390					395					400
Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly
				405					410					415	
Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser
		420						425					430		
Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly
	435						440					445			
Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
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	515						520					525			
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Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys
545					550					555					560
Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr
				565					570					575	
Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln
		580						585					590		
Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	His
	595						600					605			
Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly
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625					630					635					640
Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr
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Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro
		660						665					670		
Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala
	675						680					685			
Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser
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Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala
 705 710 715 720
 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
 805 810 815
 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
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 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

<210> 22

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22

Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser Ile
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<210> 23

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23

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 Pro Thr Met